



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/774,721

DATE: 08/20/2004

TIME: 09:06:55

Input Set : A:\Ser. No. 10 774,721 Sequence Listing.txt

Output Set: N:\CRF4\08202004\J774721.raw

3 <110> APPLICANT: JOCKERS, Ralf  
 4 COUTURIER, Cyril  
 5 UHLMANN, Eugen  
 7 <120> TITLE OF INVENTION: Oligonucleotides Which inhibit Expression of the OB-RGRP  
 Protein  
 8 And Method For Detecting Compounds Which Modify The Interaction  
 9 Between Proteins Of the OB-RGRP Family And The Leptin Receptor  
 11 <130> FILE REFERENCE: FRAV2003/0005 US NP  
 13 <140> CURRENT APPLICATION NUMBER: 10/774,721  
 14 <141> CURRENT FILING DATE: 2004-02-09  
 16 <150> PRIOR APPLICATION NUMBER: 60/461,005  
 17 <151> PRIOR FILING DATE: 2003-04-07  
 19 <150> PRIOR APPLICATION NUMBER: 0301543  
 20 <151> PRIOR FILING DATE: 2003-02-10  
 22 <160> NUMBER OF SEQ ID NOS: 47  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 648  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Homo sapiens  
 31 <400> SEQUENCE: 1  
 32 cactttatttc tgattacagt gcattgaatt tcttagaact catactatct gtatacatgt 60  
 34 gcacatgcgg cattttacta tgaaatttaa tatgctgggt tttttaatac ctttatatat 120  
 36 catgttcact ttaagaaaga cttcataagt aggagatgag ttttattctc agcaaataga 180  
 38 cctgtcaa at ttagattatg ttactcaaat tatgttactt gtttggctgt tcatgtagtc 240  
 40 acggtgctct cagaaaatat attaacgcag tctttagagg agctgccacc ttatgcagtg 300  
 42 catcgaaacc ttttgcttgg ggatgtgctt ggagaggcag ataacgctga agcaggcctc 360  
 44 tcatgaccca ggaaggccgg ggtggatccc tctttgtgtt gtagtccatg ctattaaaag 420  
 46 tgtggcccac agaccaagag cctcaacatt tcctagagcc ttattagaaa tgcagaatct 480  
 48 gaagccccac tctggaccca ggacattttg atgagatcca aaggagtgtg atgcacatga 540  
 50 aagtttgaga agcatcatca tagagaagta aacatcacac ccaacttctt tatctttcca 600  
 52 gtggctaaac cacttaacct ctctgggtgt tacctgctca tttgttta 648  
 55 <210> SEQ ID NO: 2  
 56 <211> LENGTH: 20  
 57 <212> TYPE: DNA  
 58 <213> ORGANISM: Artificial Sequence  
 60 <220> FEATURE:  
 61 <223> OTHER INFORMATION: AS14  
 63 <220> FEATURE:  
 64 <221> NAME/KEY: misc\_feature  
 65 <223> OTHER INFORMATION: antisens AS14  
 68 <400> SEQUENCE: 2  
 69 aatgccgcat gtgcacatgt 20  
 72 <210> SEQ ID NO: 3



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73 <211> LENGTH: 396
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (1)..(396)
80 <223> OTHER INFORMATION:
W--> 83 <400> 3
84 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att      48
85 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
86 1          5          10          15
88 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt      96
89 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
90          20          25          30
92 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc      144
93 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
94          35          40          45
96 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt      192
97 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
98          50          55          60
100 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct      240
101 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
102 65          70          75          80
104 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg      288
105 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
106          85          90          95
108 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca      336
109 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
110          100          105          110
112 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg      384
113 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
114          115          120          125
116 gag cag tgg tag      396
117 Glu Gln Trp
118          130
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 131
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 4
128 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
129 1          5          10          15
132 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
133          20          25          30
136 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
137          35          40          45
140 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
141          50          55          60
144 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser

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145 65          70          75          80
148 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
149          85          90          95
152 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
153          100          105          110
156 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
157          115          120          125
160 Glu Gln Trp
161          130
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 1359
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: OB RGRP LUC
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
174 <223> OTHER INFORMATION: OB RGRP LUC
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (1)..(1359)
180 <223> OTHER INFORMATION:
W--> 183 <400> 5
184 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att      48
185 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
186 1          5          10          15
188 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt      96
189 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
190          20          25          30
192 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc      144
193 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
194          35          40          45
196 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt      192
197 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
198          50          55          60
200 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct      240
201 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
202 65          70          75          80
204 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg      288
205 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
206          85          90          95
208 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca      336
209 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
210          100          105          110
212 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg      384
213 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
214          115          120          125
216 gag cag tgg att ccg ggg gat cca ccg gct aga gcc acc atg acc agc      432
217 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser

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218	130	135	140	
220	aag	gtg	tac	gac
221	Lys	Val	Tyr	Asp
222	145	150	155	160
224	tgg	tgg	gcc	agg
225	Trp	Trp	Ala	Arg
226		165	170	175
228	tac	tac	gac	agc
229	Tyr	Tyr	Asp	Ser
230		180	185	190
232	ggc	aac	gcc	gct
233	Gly	Asn	Ala	Ala
234		195	200	205
236	gag	ccc	gtg	gcc
237	Glu	Pro	Val	Ala
238		210	215	220
240	agc	ggc	aag	agc
241	Ser	Gly	Lys	Ser
242	225	230	235	240
244	tac	ctg	acc	gcc
245	Tyr	Leu	Thr	Ala
246		245	250	255
248	ttc	gtg	ggc	cac
249	Phe	Val	Gly	His
250		260	265	270
252	gag	cac	cag	gac
253	Glu	His	Gln	Asp
254		275	280	285
256	gac	gtg	atc	gag
257	Asp	Val	Ile	Glu
258		290	295	300
260	gcc	ctg	atc	aag
261	Ala	Leu	Ile	Lys
262	305	310	315	320
264	ttc	ttc	gtg	gag
265	Phe	Phe	Val	Glu
266		325	330	335
268	ccc	gag	gag	ttc
269	Pro	Glu	Glu	Phe
270		340	345	350
272	gtg	aga	aga	ccc
273	Val	Arg	Arg	Pro
274		355	360	365
276	ggc	ggc	aag	ccc
277	Gly	Gly	Lys	Pro
278		370	375	380
280	ctg	aga	gcc	agc
281	Leu	Arg	Ala	Ser
282	385	390	395	400

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284 ggc ttc ttc agc aac gcc atc gtg gag ggc gcc aag aag ttc ccc aac      1248
285 Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn
286                405                410                415
288 acc gag ttc gtg aag gtg aag ggc ctg cac ttc agc cag gag gac gcc      1296
289 Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala
290                420                425                430
292 ccc gac gag atg ggc aag tac atc aag agc ttc gtg gag aga gtg ctg      1344
293 Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val Leu
294                435                440                445
296 aag aac gag cag taa
297 Lys Asn Glu Gln
298                450
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 452
303 <212> TYPE: PRT
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: OB RGRP LUC
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <223> OTHER INFORMATION: OB RGRP LUC
313 <400> SEQUENCE: 6
315 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
316 1                5                10                15
319 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
320                20                25                30
323 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
324                35                40                45
327 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
328                50                55                60
331 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
332 65                70                75                80
335 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
336                85                90                95
339 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
340                100               105               110
343 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
344                115               120               125
347 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser
348                130               135               140
351 Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln
352 145               150               155               160
355 Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn
356                165               170               175
359 Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His
360                180               185               190
363 Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile
364                195               200               205
367 Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys

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## VERIFICATION SUMMARY

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TIME: 09:06:56

Input Set : A:\Ser. No. 10 774,721 Sequence Listing.txt

Output Set: N:\CRF4\08202004\J774721.raw

L:83 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:80  
L:183 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:180  
L:450 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:447  
L:669 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:666  
L:1147 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1144  
L:1814 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1811  
L:2433 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:2430  
L:2530 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:2527  
L:2794 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:2791